

Plant-Microbe Interfaces: The key fungal lineage of the Russulaceae, a new resource for untangling and linking beneficial plant-fungal associations and ecosystem functions

Brian Looney,¹ Marek Piatek,² Piet Jones,² Alan Kuo,³ Kerrie Barry,³ Igor Griegoriev,³ Francis Martin,¹ Dan Jacobson,² **Mitchel Doktycz,²** and **Jessy Labbé^{2*}** (Labbejj@ornl.gov)

¹INRA, Tree-Microbe Interactions, UMR1136, Champenoux, France; ²Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, TN; ³Joint Genome Institute, Walnut Creek, CA

<http://PMI.ornl.gov>

Project Goals: The goal of the PMI SFA is to understand the genome-dependent molecular and cellular events involved in establishing and maintaining beneficial interactions between plants and microbes. *Populus* and its associated microbial community serve as the experimental system for understanding how these molecular events manifest themselves within the spatially, structurally, and temporally complex scales of natural systems. To achieve this goal, we focus on 1) characterizing host and environmental drivers for diversity and function in the *Populus* microbiome, 2) utilizing microbial model system studies to elucidate *Populus*-microbial interactions at the molecular level and dissecting the signals and pathways responsible for initiating and maintaining microbial relationships and 3) develop metabolic and genomic modeling of these interactions to aid in interpreting the molecular mechanisms shaping the *Populus*-microbial interface.

The *Populus* root microbiome harbors a diverse community of ectomycorrhizal fungi (EMF) that significantly increases nutrient uptake and acquisition by the plant host while also providing protection against antagonistic parasites. Over 30 genera of EMF are known to associate with *Populus*, including many groups of mushroom-producing families including Amanitaceae, Boletaceae, Cortinariaceae, Tricholomataceae, and Russulaceae. The family Russulaceae is considered an iconic lineage of mostly mushroom-forming basidiomycetes due to their importance as edible mushrooms in many parts of the world and their ubiquity as ectomycorrhizal symbionts in both temperate and tropical forested biomes. While much research has been focused on this group, a comprehensive or cohesive synthesis by which to understand the functional diversity of the group has yet to develop. Interest in ectomycorrhizal fungi, of which Russulaceae is a key lineage, is prodigious due to the important roles they play as plant root mutualists in ecosystem functioning, global carbon sequestration, and a potential role in technology development toward environmental sustainability. As one of the most species-diverse ectomycorrhizal lineages, the Russulaceae has recently been the focus of a dense sampling and genome sequencing initiative with the Joint Genome Institute to untangle their functional roles and test whether functional niche specialization exists for independent lineages of ectomycorrhizal fungi. Here we present the reference genomes produced by this project, some comparative analyses, along with the development of co-culture systems, which are a

tremendous and promising resource for the identification of potential genetic controls for ectomycorrhizal association and decomposition.

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